Message

From: Zachary Hopkins [zrhopkin@ncsu.edu]
Sent: 4/18/2017 12:43:45 PM
To: Strynar, Mark [/o=ExchangeLabs/ou=Exchange Administrative Group (FYDIBOHF23SPDLT)/cn=Recipients/cn=5a9910d5b38e471497bd875fd329a20a-Strynar, Mark]
Subject: Question about GenX and ADONA detection limits, and PFAS method consistency

Mark,

Dr. Knappe is looking at seeing if microbes can degrade GenX and/or ADNOA. However, we we want to make sure we start at a high enough concentration that we can detect the compound in solution. What do you think the detection for amount loaded on column is? If we were to generate 50 mL of solution starting at an initial concentration of 10-50ug/L do you think we could be able to see the compound following SPE by loading 25 or 50 mL on to a wax plus cartridge?

Additionally, Dr. Knappe has been pushing me to talk to you more about he methods for the PFASs lately. I know we have talked briefly about some of the issues noticed during runs lately. However, what your thoughts were on why we see QCs and standards vary so much when run on the triple quad and created from the same stock? Is this just because there is so much drift in the machine over time? Even though we include IS which should correct, might it not be correcting for drift in signal? We have also noticed better results for the same samples on the TOF, why might that be?

I was going to try to make it by the EPA tomorrow. Maybe we can sit and talk about it more in depth. I know you typically have meetings Wednesday mornings. Would it be better to meet after lunch to chat?

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Best,
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